PCT09

RAW SEQUENCE LISTING DATE: 10/23/2001
PATENT APPLICATION: US/09/807,660A TIME: 10:13:35

Input Set : A:\09-807660 Sequence Listing.txt
Output Set: N:\CRF3\10232001\I807660A.raw

<110> APPLICANT: Maliszewski, Charles R.
Gayle III, Richard B.
Marcus, Aaron J.
Immunex Corporation
Cornell Research Foundation, Inc.
<120> TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and Recruitment
<130> FILE REFERENCE: 23,495 PCT
<140> CURRENT APPLICATION NUMBER: US 09/807,660A
<141> CURRENT FILING DATE: 2001-04-16
<150> PRIOR APPLICATION NUMBER: US 60/104,585
<151> PRIOR FILING DATE: 1998-10-16
<150> PRIOR APPLICATION NUMBER: US 60/107,466
<151> PRIOR FILING DATE: 1998-11-06
<150> PRIOR APPLICATION NUMBER: US 60/149,010
<151> PRIOR FILING DATE: 1999-08-13
<160> NUMBER OF SEQ ID NOS: 31
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO: 1
<211> LENGTH: 1599
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (67)..(1596)
<400> SEQUENCE: 1

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ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc    108
       Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
         1               5                  10
aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata   156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
 15                  20                  25                  30
gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac   204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
                 35                  40                  45
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta   252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
             50                  55                  60
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg   300
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
         65                  70                  75
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt   348
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
     80                  85                  90
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa   396
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
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68  95                  100                 105                 110
70 aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt   444
71 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
72                  115                 120                 125
74 tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa   492
75 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
76              130                 135                 140
78 gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac   540
79 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
80          145                 150                 155
82 tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa   588
83 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
84      160                 165                 170
86 ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt   636
87 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
88 175                 180                 185                 190
90 cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag   684
91 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
92                  195                 200                 205
94 gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act   732
95 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
96              210                 215                 220
98 ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa   780
99 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
100         225                 230                 235
102 ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg   828
103 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
104     240                 245                 250
106 tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att   876
107 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
108 255                 260                 265                 270
110 cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga   924
111 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
112                 275                 280                 285
114 tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc   972
115 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
116             290                 295                 300
118 aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt   1020
119 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
120         305                 310                 315
122 att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac   1068
123 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
124     320                 325                 330
126 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg   1116
127 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
128 335                 340                 345                 350
130 cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg   1164
131 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
132                 355                 360                 365
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```
134 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg   1212
135 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
136             370                 375                 380
138 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa   1260
139 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
140         385                 390                 395
142 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt   1308
143 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
144     400                 405                 410
146 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca   1356
147 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
148 415                 420                 425                 430
150 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc   1404
151 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
152                 435                 440                 445
154 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc   1452
155 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
156             450                 455                 460
158 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc   1500
159 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
160         465                 470                 475
162 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata   1548
163 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
164     480                 485                 490
166 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta   1596
167 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
168 495                 500                 505                 510
170 tag                                                           1599
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 510
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 2
179 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
180   1               5                  10                  15
182 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
183              20                  25                  30
185 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
186          35                  40                  45
188 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
189      50                  55                  60
191 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
192  65                  70                  75                  80
194 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
195                  85                  90                  95
197 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
198              100                 105                 110
200 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
201          115                 120                 125
```

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```
203 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
204     130                 135                 140
206 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
207 145                 150                 155                 160
209 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
210                 165                 170                 175
212 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
213             180                 185                 190
215 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
216         195                 200                 205
218 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
219     210                 215                 220
221 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
222 225                 230                 235                 240
224 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
225                 245                 250                 255
227 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
228             260                 265                 270
230 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
231         275                 280                 285
233 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
234     290                 295                 300
236 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
237 305                 310                 315                 320
239 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
240                 325                 330                 335
242 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
243             340                 345                 350
245 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
246         355                 360                 365
248 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
249     370                 375                 380
251 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
252 385                 390                 395                 400
254 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
255                 405                 410                 415
257 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
258             420                 425                 430
260 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
261         435                 440                 445
263 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
264     450                 455                 460
266 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
267 465                 470                 475                 480
269 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
270                 485                 490                 495
272 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
273             500                 505                 510
276 <210> SEQ ID NO: 3
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```
277 <211> LENGTH: 476
278 <212> TYPE: PRT
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
283       construct of human CD39
285 <400> SEQUENCE: 3
286 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
287   1               5                  10                  15
289 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
290              20                  25                  30
292 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
293          35                  40                  45
295 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
296      50                  55                  60
298 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
299  65                  70                  75                  80
301 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
302                  85                  90                  95
304 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
305             100                 105                 110
307 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
308         115                 120                 125
310 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
311     130                 135                 140
313 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
314 145                 150                 155                 160
316 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
317                 165                 170                 175
319 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
320             180                 185                 190
322 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
323         195                 200                 205
325 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
326     210                 215                 220
328 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
329 225                 230                 235                 240
331 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
332                 245                 250                 255
334 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
335             260                 265                 270
337 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
338         275                 280                 285
340 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
341     290                 295                 300
343 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
344 305                 310                 315                 320
346 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
347                 325                 330                 335
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 10/23/2001
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L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4